What is claimed is:

1. An isolated nucleic acid molecule comprising the coding region for a T-type calcium channel and regulatory sequences associated therewith.

2. The nucleic acid molecule of claim 1, wherein said associated regulatory sequences contain CpG-rich regions.

3. The nucleic acid molecule of claim 2, wherein the state of methylation of the CpG-rich regions is determinative of the presence of a cellular proliferative disorder in a subject from which the nucleic acid molecule is isolated.

4. The nucleic acid molecule of claim 2, wherein hypermethylation of said CpG islands is indicative of the presence of a cellular proliferative disorder in a subject from which said nucleic acid is isolated.

5. The nucleic acid molecule of claim 1, wherein said T-type calcium channel is CACNA1G.

6. The nucleic acid molecule of claim 5, wherein said nucleic acid comprises the nucleic acid sequence of SEQ ID NO: 51.

7. The nucleic acid molecule of claim 6, wherein one or more of regions 1-8 comprises methylated bases.

8. A substantially purified polypeptide encoded by the polynucleotide of SEQ ID NO:51.

9. The polypeptide of claim 8, wherein the polypeptide has an amino acid sequence as set forth in SEQ ID NO:52.

10. A method for detecting a cellular proliferative disorder in a subject comprising:
    a) contacting a nucleic acid-containing specimen from the subject with an agent that provides a determination of the methylation state of at least one gene or associated regulatory region of the gene; and
    b) identifying aberrant methylation of regions of the gene or regulatory region, wherein aberrant methylation is identified as being different when compared to the same regions of the gene or associated regulatory region in a subject not having said cellular proliferative, thereby detecting a cellular proliferative disorder in the subject.

11. The method of claim 10, wherein the regions of said gene are contained within CpG rich regions.

12. The method of claim 10, wherein the gene is selected from the group consisting of APOB, CACNA1G, CDX2, EGFR, FBN1, GPR37, HSPA6, IQGAP2, KL, PAR2, PITX2, PTCH, SDC1, SDC4 and combinations thereof.

13. The method of claim 10, wherein aberrant methylation comprises hypermethylation when compared to the same regions of the gene or associated regulatory regions in a subject not having the cellular proliferative disorder.

14. The method of claim 13, wherein the regions comprise regulatory regions of CACNA1G.

15. The method of claim 14, wherein the regions comprise regions 1-8 of CACNA1G.

16. The method of claim 15, wherein the regions comprise regions 1-2 of CACNA1G.

17. The method of claim 15, wherein the regions comprise regions 5-7 of CACNA1G.

18. The method of claim 15, wherein the regions comprise regions 4 and 8 of CACNA1G.

19. The method of claim 10, wherein the agent is a pair of primers that hybridize with a target sequence in the gene or associated regulatory region of the gene.

20. The method of claim 19, wherein the primers hybridize with a target polynucleotide sequence having the sequence selected from the group consisting of SEQ ID NO:55-103 and SEQ ID NO:104.

21. The method of claim 20, wherein the primers are in consecutive pairs selected from the group consisting of SEQ ID NO:1-49 and SEQ ID NO:50.

22. The method of claim 10, wherein the nucleic acid-containing specimen comprises a tissue selected from the group consisting of brain, colon, urogenital, lung, renal, prostate, pancreas, liver, esophagus, stomach, hematopoietic, breast, thymus, testis, ovarian, and uterine.

23. The method of claim 10, wherein the nucleic acid-containing specimen is selected from the group consisting of serum, urine, saliva, blood, cerebrospinal fluid, pleural fluid, ascites fluid, sputum, stool, and biopsy sample.

24. The method of claim 10, wherein said cellular proliferative disorder is selected from the group consisting of low grade astrocytoma, anaplastic astrocytoma, glioblastoma, medulloblastoma, gastric cancer, colorectal cancer, colorectal adenoma, acute myelogenous leukemia, lung cancer, renal cancer, leukemia, breast cancer, prostate cancer, endometrial cancer and neuroblastoma.

25. A kit useful for the detection of a cellular proliferative disorder in a subject comprising:

a) carrier means compartmentalized to receive a sample therein;

b) one or more containers comprising a first container containing a reagent which modifies unmethylated cytosine and a second container containing primers for amplification of a CpG-containing nucleic acid, wherein the primer hybridizes with a target polynucleotide sequence having the sequence selected from the group consisting of SEQ ID NO:55-103 and SEQ ID NO:104.

26. The kit of claim 25, further comprising a third container containing a methylation sensitive restriction endonuclease.

27. The kit of claim 25, wherein said modifying reagent is bisulfite.

28. The kit of claim 25, wherein the primers are selected from the group consisting of SEQ ID NO:1-49 and SEQ ID NO:50.

29. Isolated oligonucleotide primer(s) for detection of a methylated CpG-containing nucleic acid wherein the primer hybridizes with a target polynucleotide sequence having the sequence selected from the group consisting of SEQ ID NO:55-103 and SEQ ID NO:104.

30. The primers of claim 29, wherein said primers are selected from the group consisting of SEQ ID NO:1-49 and SEQ ID NO:50.

31. An isolated nucleic acid molecule having at least one methylated Cytosine of a CpG dinucleotide in a CpG-rich region and encoding a gene selected from the group consisting of APOB, CACNA1G, CDX2, EGFR, FBN1, GPR37, HSPA6, IQGAP2, KL, PAR2, PITX2, PTCH, SDC1, and SDC4.

32. The nucleic acid molecule of claim 31, wherein the methylated C residue of a CpG dinucleotide is located within a CpG-rich region selected from the group consisting of SEQ ID NO:105-118 and SEQ ID NO:119.

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